

R. Landson

1647

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/287,332

DATE: 09/26/2000

TIME: 08:40:36

Input Set : A:\16777309.app

Output Set: N:\CRF3\09262000\I287332.raw

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OCT 02 2000

TECH CENTER 1600/2900

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3 <110> APPLICANT: GAUTVIK, KAARE M.
4 ALSTROM, PETER
5 OYEN, TORDIS B.
6 GABRIELSEN, ODD S.
8 <120> TITLE OF INVENTION: PRODUCTION OF HUMAN PARATHYROID HORMONE FROM
9 MICROORGANISMS
11 <130> FILE REFERENCE: 16777/309
13 <140> CURRENT APPLICATION NUMBER: 09/287,332
C--> 14 <141> CURRENT FILING DATE: 2000-04-07
16 <160> NUMBER OF SEQ ID NOS: 25
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 348
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <223> OTHER INFORMATION: "n" bases at various positions throughout the sequence
27 represent a, g, c, or t
29 <400> SEQUENCE: 1
W--> 30 atgathccng cnaargayat ggcnaargtn atgathgtna tgytngcnat htgyttyytn 60
W--> 31 acnaarwsng ayggnaarws ngtnaaraar mgnwsngtnw sngarathca rytnatgcay 120
W--> 32 aayytnggna arcayytnaa ywsnatggar mngtngart ggytnmgnaa raarytnear 180
W--> 33 gaygtncaya ayttygtngc nytngngncc cnytngcnc cnmgngaygc nggnwsncar 240
W--> 34 mgncnmgna araargarga yaaygtnytn gtngarwsnc aygaraarws nytnggngar 300
W--> 35 gcngayaarg cngaygtnaa ygtnytnacn aargcnaarw sncartrr 348
38 <210> SEQ ID NO: 2
39 <211> LENGTH: 351
40 <212> TYPE: DNA
41 <213> ORGANISM: Homo sapiens
43 <400> SEQUENCE: 2
44 atgatgatac ctgcaaaaaga catggctaaa gttatgattg tcatgttggc aatttgtttt 60
45 cttacaaaat cggatgggaa atctgttaag aagagatctg tgagtgaat acagcttatg 120
46 cataacctgg gaaaacatct gaactcgatg gagagagtag aatggctgcg taagaagctg 180
47 caggatgtgc acaattttgt tgcccttgga gctcctctag ctcccagaga tgctggttcc 240
48 cagaggcccc gaaaaaagga agacaatgtc ttggttgaga gccatgaaaa aagtcttgga 300
49 gaggcagaca aagctgatgt gaatgtatta actaaagcta aatcccagtg a 351
52 <210> SEQ ID NO: 3
53 <211> LENGTH: 432
54 <212> TYPE: DNA
55 <213> ORGANISM: Homo sapiens
57 <220> FEATURE:
58 <223> OTHER INFORMATION: "n" bases at various positions throughout the sequence
59 represent a, g, c, or t
61 <400> SEQUENCE: 3
W--> 62 tatgatgath ccngcnaarg ayatggcnaa rgtnatgath gtnatgytng cnathtgytt 60
W--> 63 yytnacnaar wsngayggna arwsngtnaa raarmgnwsn gtnwsngara thcarytnat 120
W--> 64 gcayaayytn ggnaarcayy tnaaywsnat ggarmgngtn gartggytnm gnaaraaryt 180
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W--> 65 ncargaygtg cayaaytttg tngcnytnng ngcncnytn gcncnmgng aygcnggnws 240
W--> 66 ncarmgnccn mgnaaraarg argayaaygt nytngtngar wsncaygara arwsnytnng 300
W--> 67 ngargcngay aargcngayg tnaaygtnyt nacnaargcn aarwsncart rraaatgaaa 360
68 acagatatgg tcagagtgtc gctctagaca gtgtagggca acaatacatg ctgctaattc 420
69 aaagctctat ta 432
72 <210> SEQ ID NO: 4
73 <211> LENGTH: 432
74 <212> TYPE: DNA
75 <213> ORGANISM: Homo sapiens
77 <400> SEQUENCE: 4
78 tatgatgata cctgcaaaag acatggctaa agttatgatt gtcatgttgg caatttgttt 60
79 tcttacaaaa tcggatggga aatctgttaa gaagagatct gtgagtgaag tacagcttat 120
80 gcataacctg ggaacacatc tgaactcgat ggagagagta gaatggctgc gtaagaagct 180
81 gcaggatgtg cacaattttg ttgcccttgg agctcctcta gctcccagag atgctggttc 240
82 ccagaggccc cgaaaaaagg aagacaatgt cttggttgag agccatgaaa aaagtcttgg 300
83 agaggcagac aaagctgatg tgaatgtatt aactaaagct aaatcccagt gaaaatgaaa 360
84 acagatatgg tcagagtgtc gctctagaca gtgtagggca acaatacatg ctgctaattc 420
85 aaagctctat ta 432
88 <210> SEQ ID NO: 5
89 <211> LENGTH: 432
90 <212> TYPE: DNA
91 <213> ORGANISM: Homo sapiens
93 <220> FEATURE:
94 <221> NAME/KEY: CDS
95 <222> LOCATION: (5)..(349)
97 <400> SEQUENCE: 5
98 tatg atg ata cct gca aaa gac atg gct aaa gtt atg att gtc atg ttg 49
99 Met Ile Pro Ala Lys Asp Met Ala Lys Val Met Ile Val Met Leu
100 1 5 10 15
102 gca att tgt ttt ctt aca aaa tcg gat ggg aaa tct gtt aag aag aga 97
103 Ala Ile Cys Phe Leu Thr Lys Ser Asp Gly Lys Ser Val Lys Lys Arg
104 20 25 30
106 tct gtg agt gaa ata cag ctt atg cat aac ctg gga aaa cat ctg aac 145
107 Ser Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu Asn
108 35 40 45
110 tcg atg gag aga gta gaa tgg ctg cgt aag aag ctg cag gat gtg cac 193
111 Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val His
112 50 55 60
114 aat ttt gtt gcc ctt gga gct cct cta gct ccc aga gat gct ggt tcc 241
115 Asn Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp Ala Gly Ser
116 65 70 75
118 cag agg ccc cga aaa aag gaa gac aat gtc ttg gtt gag agc cat gaa 289
119 Gln Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val Glu Ser His Glu
120 80 85 90 95
122 aaa agt ctt gga gag gca gac aaa gct gat gtg aat gta tta act aaa 337
123 Lys Ser Leu Gly Glu Ala Asp Lys Ala Asp Val Asn Val Leu Thr Lys
124 100 105 110
126 gct aaa tcc cag tgaaaatgaa aacagatatg gtcagagtgc tgctctagac 389
127 Ala Lys Ser Gln

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128          115
130 agtgtagggc aacaatacat gctgctaatt caaagctcta tta          432
133 <210> SEQ ID NO: 6
134 <211> LENGTH: 115
135 <212> TYPE: PRT
136 <213> ORGANISM: Homo sapiens
138 <400> SEQUENCE: 6
139 Met Ile Pro Ala Lys Asp Met Ala Lys Val Met Ile Val Met Leu Ala
140   1          5          10          15
142 Ile Cys Phe Leu Thr Lys Ser Asp Gly Lys Ser Val Lys Lys Arg Ser
143          20          25          30
145 Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu Asn Ser
146          35          40          45
148 Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val His Asn
149          50          55          60
151 Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp Ala Gly Ser Gln
152          65          70          75          80
154 Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val Glu Ser His Glu Lys
155          85          90          95
157 Ser Leu Gly Glu Ala Asp Lys Ala Asp Val Asn Val Leu Thr Lys Ala
158          100          105          110
160 Lys Ser Gln
161          115
165 <210> SEQ ID NO: 7
166 <211> LENGTH: 874
167 <212> TYPE: DNA
168 <213> ORGANISM: Homo sapiens
170 <220> FEATURE:
171 <223> OTHER INFORMATION: MFal-hPTH fusion gene
173 <400> SEQUENCE: 7
174 agtgcaagaa aacccaaaag caacaacagg ttttggataa gtacatatat aagagggcct 60
175 tttgttccca tcaaaaatgt tactgttctt acgattcatt tacgattcaa gaatagttca 120
176 aacaagaaga ttacaaacta tcaatttcat acacaatata aacgacccaa agaatgagat 180
177 ttccttcaat ttttactgca gttttattcg cagcatcctc cgcattagct gctccagtca 240
178 acactacaac agaagatgaa acggcacaaa ttccggctga agctgtcatc ggttactcag 300
179 atttagaagg ggatttcgat gttgctgttt tgccattttc caacagcaca aataacgggt 360
180 tattgtttat aaatactact attgccagca ttgctgctaa agaagaaggg gtatctttgg 420
181 ataaaagaga ggctgaagct tctgtgagtg aaatacagct tatgcataac ctgggaaaac 480
182 atctgaactc gatggagaga gtagaatggc tgcgtaagaa gctgcaggat gtgcacaatt 540
183 ttgttgccct tggagctcct ctagctccca gagatgctgg ttcccagagg ccccgaaaaa 600
184 aggaagacaa tgtcttgggt gagagccatg aaaaaagtct tggagaggca gacaaaagctg 660
185 atgtgaatgt attaaactaa gctaaatccc agtgaaaatg aaaacagata ttgtcagagt 720
186 tctgctctag agtcgacttt gttcccactg tacttttagc tcgtacaaaa tacaatatat 780
187 ttttcatttc tccgtaaaac acctgttttc ccatgtaata tccttttcta tttttcgttt 840
188 cgttaccaac ttacacata ctttatatag ctat          874
191 <210> SEQ ID NO: 8
192 <211> LENGTH: 874
193 <212> TYPE: DNA
194 <213> ORGANISM: Homo sapiens

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196 <220> FEATURE:
197 <223> OTHER INFORMATION: MFA1-hPTH fusion gene
199 <220> FEATURE:
200 <223> OTHER INFORMATION: "n" bases at various positions throughout the sequence
201     represent a, g, c, or t
203 <400> SEQUENCE: 8
204 agtgcaagaa aacacaaaag caacaacagg ttttggataa gtacatatat aagagggcct 60
205 tttgttccca tcaaaaatgt tactgttctt acgattcatt tacgattcaa gaatagttoa 120
206 aacaagaaga ttacaaacta tcaatttcat acacaatata aacgaccaa agaatgagat 180
207 ttccttcaat ttttactgca gttttattcg cagcatcctc cgcattagct gctccagtca 240
208 aactacaac agaagatgaa acggcacaaa ttccggctga agctgtcatc ggttactcag 300
209 atttagaagg ggatttcgat gttgctgttt tgccattttc caacagcaca aataacgggt 360
210 tattgtttat aaatactact attgccagca ttgctgctaa agaagaaggg gtatctttgg 420
W--> 211 ataaaaagaga ggctgaagct wsngtnwsng arathcaryt natgcayaay ytnngnaarc 480
W--> 212 ayytnaayws natggarmgn gtngartggy tnmgnaaraa rytncargay gtncaayaay 540
W--> 213 tygtngcnyt ngngncncn ytnncncnm gngaygcngg nwsncarmgn ccnmgnaara 600
W--> 214 argargayaa ygtnyngtn garwsncayg araarwsnyt ngngngargcn gayaargcng 660
W--> 215 ayytnaaygt nytnacnaar gcnaarwsnc artrraaatg aaaacagata ttgtcagagt 720
216 tctgctctag agtcgacttt gttccactg tacttttagc tcgtacaaaa tacaatatat 780
217 ttttcatttc tccgtaaaca acctgttttc ccatgtaata tctttttcta ttttcggtt 840
218 cgttaccaac ttacacata ctttatatag ctat 874
221 <210> SEQ ID NO: 9
222 <211> LENGTH: 18
223 <212> TYPE: DNA
224 <213> ORGANISM: Artificial Sequence
226 <220> FEATURE:
227 <223> OTHER INFORMATION: Description of Artificial Sequence:
228     Oligonucleotide
230 <400> SEQUENCE: 9
231 ggctgcgtca gaagctgc 18
234 <210> SEQ ID NO: 10
235 <211> LENGTH: 24
236 <212> TYPE: DNA
237 <213> ORGANISM: Artificial Sequence
239 <220> FEATURE:
240 <223> OTHER INFORMATION: Description of Artificial Sequence:
241     Oligonucleotide
243 <400> SEQUENCE: 10
244 tactatggac gttttctgta ccga 24
247 <210> SEQ ID NO: 11
248 <211> LENGTH: 24
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: Description of Artificial Sequence:
254     Oligonucleotide
256 <400> SEQUENCE: 11
257 ctcaagacga gatctgtcac atcc 24
260 <210> SEQ ID NO: 12

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261 <211> LENGTH: 30
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Description of Artificial Sequence:
267     Oligonucleotide
269 <400> SEQUENCE: 12
270 gatcagatct gcaggatgga tccaaagctt          30
273 <210> SEQ ID NO: 13
274 <211> LENGTH: 30
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: Description of Artificial Sequence:
280     Oligonucleotide
282 <400> SEQUENCE: 13
283 tctagacgtc ctacctaggt ttcgaactag          30
286 <210> SEQ ID NO: 14
287 <211> LENGTH: 22
288 <212> TYPE: DNA
289 <213> ORGANISM: Artificial Sequence
291 <220> FEATURE:
292 <223> OTHER INFORMATION: Description of Artificial Sequence:
293     Oligonucleotide
295 <400> SEQUENCE: 14
296 tggcattggc tgcaactaaa gc                  22
299 <210> SEQ ID NO: 15
300 <211> LENGTH: 4
301 <212> TYPE: PRT
302 <213> ORGANISM: Homo sapiens
304 <400> SEQUENCE: 15
305 Glu Ala Glu Ala
306     1
309 <210> SEQ ID NO: 16
310 <211> LENGTH: 18
311 <212> TYPE: DNA
312 <213> ORGANISM: Artificial Sequence
314 <220> FEATURE:
315 <223> OTHER INFORMATION: Description of Artificial Sequence:
316     Oligonucleotide
318 <400> SEQUENCE: 16
319 ggataaaaaga tctgtgag                      18
322 <210> SEQ ID NO: 17
323 <211> LENGTH: 18
324 <212> TYPE: DNA
325 <213> ORGANISM: Artificial Sequence
327 <220> FEATURE:
328 <223> OTHER INFORMATION: Description of Artificial Sequence:
329     Oligonucleotide

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Input Set : A:\16777309.app
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L:30 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:30 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:30 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:31 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:31 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
M:340 Repeated in SeqNo=1
L:32 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:32 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
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L:62 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:62 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:62 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
L:63 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:63 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
M:340 Repeated in SeqNo=3
L:64 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
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L:211 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
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L:212 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:212 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
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